no location
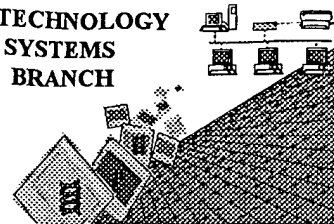
RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _10/619,359_

Source: _OIPE_

Date Processed by STIC: _7/28/2003_

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1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , EFS Submission **User Manual** - ePAVE)
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Revised 04/24/2003

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OIPE

RAW SEQUENCE LISTING   DATE: 07/28/2003
PATENT APPLICATION: **US/10/619,359**   TIME: 08:59:07

Input Set : **A:\G00307-70020.txt**
Output Set: **N:\CRF4\07282003\J619359.raw**

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      4 <110> APPLICANT: STOCKER, PENNY J.
      5         STEIMEL-CRESPI, DOROTHY T.
      6         CRESPI, CHARLES L.
      9 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
     12 <130> FILE REFERENCE: G00307.70020.US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/619,359
C--> 14 <141> CURRENT FILING DATE: 2003-07-14
     14 <150> PRIOR APPLICATION NUMBER: US 60/156,921
     15 <151> PRIOR FILING DATE: 1999-09-28
     17 <150> PRIOR APPLICATION NUMBER: US 60/158,818
     18 <151> PRIOR FILING DATE: 1999-10-12
     20 <150> PRIOR APPLICATION NUMBER: US 09/672,810
     21 <151> PRIOR FILING DATE: 2000-09-28
     23 <160> NUMBER OF SEQ ID NOS: 18
     25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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     28 <211> LENGTH: 4186
     29 <212> TYPE: DNA
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     39                                               Met Asp Leu Glu Gly
     40                                                1                5
     42  gac cgc aat gga gga gca gag aag aag aac ttt ttt aaa ctg aac aat     162
     43  Asp Arg Asn Gly Gly Ala Glu Lys Lys Asn Phe Phe Lys Leu Asn Asn
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     46  aaa agt aaa aaa gat aag aag gaa agg aaa cca act gtc agt gta ttt     210
     47  Lys Ser Lys Lys Asp Lys Lys Glu Arg Lys Pro Thr Val Ser Val Phe
     48              25              30              35
     50  tca atg ttt cgc tat tca aat tgg ctt gac aag ttg tat atg gtg gtg     258
     51  Ser Met Phe Arg Tyr Ser Asn Trp Leu Asp Lys Leu Tyr Met Val Val
     52          40              45              50
     54  gga act ttg gct gcc atc atc cat gga gct gga ctt cct ctc atg atg     306
     55  Gly Thr Leu Ala Ala Ile Ile His Gly Ala Gly Leu Pro Leu Met Met
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ᴾᴾ 5-6

RAW SEQUENCE LISTING   DATE: 07/28/2003
PATENT APPLICATION: US/10/619,359   TIME: 08:59:07

Input Set : A:\G00307-70020.txt
Output Set: N:\CRF4\07282003\J619359.raw

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59  Leu Val Phe Gly Asp Met Thr Asp Thr Phe Ala Asn Ala Gly Asn Leu
60   70              75                  80                  85

62  gga gat tta gga gct ctg ttg act aat agc agt aat atc act gat aca    402
63  Gly Asp Leu Gly Ala Leu Leu Thr Asn Ser Ser Asn Ile Thr Asp Thr
64           90                  95                  100

66  gtg ccc gtc atg aat ctg gag gaa gat atg acc agg tat gcc tat tat    450
67  Val Pro Val Met Asn Leu Glu Glu Asp Met Thr Arg Tyr Ala Tyr Tyr
68          105                 110                 115

70  tac agt gga att ggt gct ggg gtg ctg gtt gct gct tac att cag gtt    498
71  Tyr Ser Gly Ile Gly Ala Gly Val Leu Val Ala Ala Tyr Ile Gln Val
72          120                 125                 130

74  tca ttt tgg tgc ctg gca gct gga aga caa ata cac aaa att aga aaa    546
75  Ser Phe Trp Cys Leu Ala Ala Gly Arg Gln Ile His Lys Ile Arg Lys
76      135                 140                 145

78  cag ttt ttt cat gct ata atg cga cag gag ata ggc tgg ttt gat gtg    594
79  Gln Phe Phe His Ala Ile Met Arg Gln Glu Ile Gly Trp Phe Asp Val
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82  cac gat gtt ggg gag ctt aac acc cgg ctt aca gat gat gtc tcc aag    642
83  His Asp Val Gly Glu Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys
84          170                 175                 180

86  att aat gaa gga att ggt gac aaa att gga atg ttc ttt cag tca atg    690
87  Ile Asn Glu Gly Ile Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Met
88          185                 190                 195

90  gca aca ttt ttc act ggg ttt ata gta gga ttt aca cgt ggt tgg aag    738
91  Ala Thr Phe Phe Thr Gly Phe Ile Val Gly Phe Thr Arg Gly Trp Lys
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94  cta acc ctt gtg att ttg gcc atc agt cct gtt ctt gga ctg tca gct    786
95  Leu Thr Leu Val Ile Leu Ala Ile Ser Pro Val Leu Gly Leu Ser Ala
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98  gca gtc tgg gca aag ata ctg tct tca ttt act gat aaa gaa ctc tta    834
99  Ala Val Trp Ala Lys Ile Leu Ser Ser Phe Thr Asp Lys Glu Leu Leu
100 230                 235                 240                 245

102 gct tat gca aaa gct gga gca gta gct gaa gag gtc ttg gca gca att    882
103 Ala Tyr Ala Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile
104             250                 255                 260

106 aga act gtg att gca ttt gga gga caa aag aaa gaa ctc gaa agg tac    930
107 Arg Thr Val Ile Ala Phe Gly Gly Gln Lys Lys Glu Leu Glu Arg Tyr
108             265                 270                 275

110 aac aaa aat tta gaa gaa gct aaa aga att ggg ata aag aaa gct att    978
111 Asn Lys Asn Leu Glu Glu Ala Lys Arg Ile Gly Ile Lys Lys Ala Ile
112             280                 285                 290

114 aca gcc aat att tct ata ggt gct gct ttc ctg ctt atc tat gca tct    1026
115 Thr Ala Asn Ile Ser Ile Gly Ala Ala Phe Leu Leu Ile Tyr Ala Ser
116     295                 300                 305

118 tat gct ctg gcc ttc tgg tat ggg acc acc ttg gtc ctc tca aag gaa    1074
119 Tyr Ala Leu Ala Phe Trp Tyr Gly Thr Thr Leu Val Leu Ser Lys Glu
120 310                 315                 320                 325

122 tat tct att gga caa gta ctc act gta ttc ttt tct gta tta att ggg    1122
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```
123  Tyr Ser Ile Gly Gln Val Leu Thr Val Phe Phe Ser Val Leu Ile Gly
124                  330             335             340
126  gct ttt agt gtt gga cag gca tct cca agc att gaa gca ttt gca aat    1170
127  Ala Phe Ser Val Gly Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn
128                  345             350             355
130  gca aga gga gca gct ttt gaa atc ttc aag ata att gat aat aag cca    1218
131  Ala Arg Gly Ala Ala Phe Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro
132                  360             365             370
134  agt att gac agc tat tcg aag agt ggg cac aaa cca gat aat att aag    1266
135  Ser Ile Asp Ser Tyr Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys
136              375             380             385
138  gga aat ttg gaa ttc aga aat gtt cac ttc agt tac cca tct cga aaa    1314
139  Gly Asn Leu Glu Phe Arg Asn Val His Phe Ser Tyr Pro Ser Arg Lys
140  390             395             400             405
142  gaa gtt aag atc ttg aag ggc ctg aac ctg aag gtg cag agt ggg cag    1362
143  Glu Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln
144                  410             415             420
146  acg gtg gcc ctg gtt gga aac agc ggc tgt ggg aag agc aca acg gtc    1410
147  Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val
148                  425             430             435
150  cag ctg atg cag agg ctt tat gac ccc aca gag ggc atg gtc agt gtt    1458
151  Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr Glu Gly Met Val Ser Val
152                  440             445             450
154  gat gga cag gat att agg acc ata aac gta agg ttt cta cgg gaa atc    1506
155  Asp Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Phe Leu Arg Glu Ile
156              455             460             465
158  atc ggt gtg gtg agt cag gaa cct gta ttg ttt gcc acc acg ata gct    1554
159  Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala
160  470             475             480             485
162  gaa aac att cgc tat ggt cgt gaa gat gtc acc atg gat gag att gag    1602
163  Glu Asn Ile Arg Tyr Gly Arg Glu Asp Val Thr Met Asp Glu Ile Glu
164                  490             495             500
166  aaa gct gtc aag gaa gcc aat gcc tat gac ttt atc atg aaa ctg cct    1650
167  Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro
168                  505             510             515
170  cag aaa ttt gac acc ctg gtt gga gag aga ggg gcc cag ctg agt ggt    1698
171  Gln Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly
172                  520             525             530
174  ggg cag aag cag agg atc gcc att gca cgt gcc ctg gtt cgc aac ccc    1746
175  Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro
176              535             540             545
178  aag atc ctc ctg ctg gac gag gcc acg tca gcc ttg gac aca gaa agt    1794
179  Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
180  550             555             560             565
182  gaa gca gtg gtt cag gtg gct ctg gat aag gcc aga aaa ggt cgg acc    1842
183  Glu Ala Val Val Gln Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr
184                  570             575             580
186  acc att gtg ata gct cat cgt ttg tct acg gtt cgt aat gcc gac gtc    1890
187  Thr Ile Val Ile Ala His Arg Leu Ser Thr Val Arg Asn Ala Asp Val
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188             585                590                595
190   atc gct ggt ttc gat gat gga gtc att gtg gag aaa gga aat cat gat      1938
191   Ile Ala Gly Phe Asp Asp Gly Val Ile Val Glu Lys Gly Asn His Asp
192           600                605                610
194   gag ctc atg aaa gag aaa ggc att tac ttc aaa ctt gtc aca atg cag      1986
195   Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln
196           615                620                625
198   aca gca gga aat gaa att gaa tta gaa aat gca gct gat gaa tcc aaa      2034
199   Thr Ala Gly Asn Glu Ile Glu Leu Glu Asn Ala Ala Asp Glu Ser Lys
200   630                635                640                645
202   agt gaa att gat acc ttg gaa atg tct tca cat gat tca gga tcc agt      2082
203   Ser Glu Ile Asp Thr Leu Glu Met Ser Ser His Asp Ser Gly Ser Ser
204           650                655                660
206   cta ata aga aaa aga tcc act cgt agg agt gtc cgt gga tca caa ggc      2130
207   Leu Ile Arg Lys Arg Ser Thr Arg Arg Ser Val Arg Gly Ser Gln Gly
208           665                670                675
210   caa gac aga aag ctt agt acc aaa gag gct ctg gat gaa agt ata cct      2178
211   Gln Asp Arg Lys Leu Ser Thr Lys Glu Ala Leu Asp Glu Ser Ile Pro
212           680                685                690
214   cca gtt tcc ttt tgg agg att atg aag cta aat tta act gag tgg cct      2226
215   Pro Val Ser Phe Trp Arg Ile Met Lys Leu Asn Leu Thr Glu Trp Pro
216           695                700                705
218   tat ttt gtt gtt ggt gta ttt tgt gcc att ata aat gga ggt ctg caa      2274
219   Tyr Phe Val Val Gly Val Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln
220   710                715                720                725
222   cca gca ttt gca gta ata ttt tca aag att ata ggg att ttt aca aga      2322
223   Pro Ala Phe Ala Val Ile Phe Ser Lys Ile Ile Gly Ile Phe Thr Arg
224           730                735                740
226   aat gat gat gcc gaa aca aaa cga cag aat agt aac ttg ttt tca cta      2370
227   Asn Asp Asp Ala Glu Thr Lys Arg Gln Asn Ser Asn Leu Phe Ser Leu
228           745                750                755
230   ttg ttt cta gtc ctt gga att gtt tct ttt att aca ttt ttc ctt cag      2418
231   Leu Phe Leu Val Leu Gly Ile Val Ser Phe Ile Thr Phe Phe Leu Gln
232           760                765                770
234   ggc ttc aca ttt ggc aaa gct gga gag atc ctc acc aag cgg ctc cga      2466
235   Gly Phe Thr Phe Gly Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg
236           775                780                785
238   tac atg gtt ttc cga tcc atg ctc aga cag gat gtg agc tgg ttt gat      2514
239   Tyr Met Val Phe Arg Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp
240   790                795                800                805
242   gac cct aaa aac acc act gga gca ttg act acc agg ctc gcc aat gat      2562
243   Asp Pro Lys Asn Thr Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp
244           810                815                820
246   gct gct caa gtt aaa ggg gct ata ggt tcc agg ctt gct ata att acc      2610
247   Ala Ala Gln Val Lys Gly Ala Ile Gly Ser Arg Leu Ala Ile Ile Thr
248           825                830                835
250   cag aat ata gca aat ctt ggg aca gga ata att ata tcc tta atc tat      2658
251   Gln Asn Ile Ala Asn Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr
252           840                845                850
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RAW SEQUENCE LISTING   DATE: 07/28/2003
PATENT APPLICATION: US/10/619,359   TIME: 08:59:07

Input Set : A:\G00307-70020.txt
Output Set: N:\CRF4\07282003\J619359.raw

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256            855                 860             865
258   ata gca gga gtt gtt gaa atg aaa atg ttg tct gga caa gca ctg aaa      2754
259   Ile Ala Gly Val Val Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys
260   870                 875             880                 885
262   gat aag aaa gaa cta gaa ggt gct ggg aag atc gct act gaa gca ata      2802
263   Asp Lys Lys Glu Leu Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile
264                 890                 895                 900
266   gaa aac ttc cga act gtt gtt tct ttg act cag gag cag aag ttt gaa      2850
267   Glu Asn Phe Arg Thr Val Val Ser Leu Thr Gln Glu Gln Lys Phe Glu
268            905                 910                 915
270   cat atg tat gat cag agt ttg cag gta cca tac aga aac tct ttg agg      2898
271   His Met Tyr Asp Gln Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg
272            920                 925             930
274   aaa gca cac atc ttt gga atc acg ttt tcc ttc acg cag gca atg atg      2946
275   Lys Ala His Ile Phe Gly Ile Thr Phe Ser Phe Thr Gln Ala Met Met
276            935                 940             945
278   tat ttt tcc tat gct gga tgt ttc cgg ttt gga gcc tac ttg gtg gca      2994
279   Tyr Phe Ser Tyr Ala Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala
280   950                 955             960                 965
282   cat agt ctc atg agc ttt gag gat gtt ctg tta gta ttt tca gct gtt      3042
283   His Ser Leu Met Ser Phe Glu Asp Val Leu Leu Val Phe Ser Ala Val
284            970                 975             980
286   gtc ttt ggt gcc atg gcc gtg ggg caa gtc agt tca ttt gct cct gac      3090
287   Val Phe Gly Ala Met Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp
288            985                 990             995
290   tat gcc aaa gcc aaa gta tca gca gcc cac atc atc atg atc att gaa      3138
291   Tyr Ala Lys Ala Lys Val Ser Ala Ala His Ile Ile Met Ile Ile Glu
292            1000                1005            1010
294   aaa acc cct ttg att gac agc tac agc aca gaa ggc cta aag ccg aac      3186
295   Lys Thr Pro Leu Ile Asp Ser Tyr Ser Thr Glu Gly Leu Lys Pro Asn
296      1015                1020            1025
298   aca ttg gaa gga aat gtc aca ttt aat gaa gtt gta ttc aac tat ccc      3234
299   Thr Leu Glu Gly Asn Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro
W-->300   (030) 1030            1035                1040                1045
302   acc cga ctg gac atc cca gtg ctt cag ggg ctg agc ctg gaa gtg aag      3282
303   Thr Arg Leu Asp Ile Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys
304            1050                1055            1060
306   aag ggc cag acg ctg gcc ctg gtg ggc agc agt ggc tgt ggg aag agc      3330
307   Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser
308            1065                1070            1075
310   acg gtg gtc cag ctc ctg gag cgg ttc tat gac ccc ttg gcg ggg aaa      3378
311   Thr Val Val Gln Leu Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Lys
312            1080                1085            1090
314   gtg ctg ctt gac ggc aaa gaa ata aag caa ctg aat gtt cag tgg ctc      3426
315   Val Leu Leu Asp Gly Lys Glu Ile Lys Gln Leu Asn Val Gln Trp Leu
316      1095                1100            1105
318   cga gca cac ctg ggc atc gtg tcc cag gag ccc atc ctg ttt gac tgc      3474
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When numbering the first amino acid on a line, begin the number directly under the first letter of the amino acid

e.g. Thr Ser
1030 Ala Leu

7/28/03

RAW SEQUENCE LISTING   DATE: 07/28/2003
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Input Set : A:\G00307-70020.txt
Output Set: N:\CRF4\07282003\J619359.raw

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      322  agc att agt gag aac att gcc tat gga gac aac agc cgg gtg gtg tca   3522
      323  Ser Ile Ser Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser
      324                  1130              1135              1140
      326  cag gaa gag atc gtg agg gca gcc aag gag gcc aat ata cac gcc ttc   3570
      327  Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala Asn Ile His Ala Phe
      328              1145              1150              1155
      330  atc gag tca ctg cct aat aaa tat agc acc aga gta gga gac aaa gga   3618
      331  Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Arg Val Gly Asp Lys Gly
      332          1160              1165              1170
      334  act cag ctc tct ggt ggc cag aaa caa cgc att gcc ata gct cgt gcc   3666
      335  Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala
      336      1175              1180              1185
      338  ctt gtt aga cag cct cat att ttg ctt ttg gat gaa gcc aca tca gct   3714
      339  Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala
W-->  340  (190)1190              1195              1200              1205
      342  ctg gat aca gaa agt gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc   3762
      343  Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala
      344                  1210              1215              1220
      346  aga gaa ggc cgt acc tgc att gtg att gct cac cgc ctg tcc acc atc   3810
      347  Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile
      348              1225              1230              1235
      350  cag aat gca gac tta ata gtg gtg ttt cag aat ggc aga gtc aag gag   3858
      351  Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly Arg Val Lys Glu
      352          1240              1245              1250
      354  cac ggc aca cat cag cag ctg ctg gca cag aaa ggc atc tat ttt tca   3906
      355  His Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser
      356      1255              1260              1265
      358  atg gtc agt gtc cag gct gga gca aag cgc cag t gaactgtgac            3950
      359  Met Val Ser Val Gln Ala Gly Ala Lys Arg Gln
W-->  360  (270)1270              1275              1280
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      364  tcagagtctt cagacactcg taattaaagg aagagagcga gagacatcat caagtggaga  4130
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      546                                              Met Asp Leu Glu Gly
      547                                              1               5
      549  gac cgc aat gga gga gca gag aag aag aac ttt ttt aaa ctg aac aat    162
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551              10                  15                  20
553  aaa agt aaa aaa gat aag aag gaa agg aaa cca act gtc agt gta ttt       210
554  Lys Ser Lys Lys Asp Lys Lys Glu Arg Lys Pro Thr Val Ser Val Phe
555              25                  30                  35
557  tca atg ttt cgc tat tca aat tgg ctt gac aag ttg tat atg gtg gtg       258
558  Ser Met Phe Arg Tyr Ser Asn Trp Leu Asp Lys Leu Tyr Met Val Val
559              40                  45                  50
561  gga act ttg gct gcc atc atc cat gga gct gga ctt cct ctc atg atg       306
562  Gly Thr Leu Ala Ala Ile Ile His Gly Ala Gly Leu Pro Leu Met Met
563              55                  60                  65
565  ctg gtg ttt gga gac atg acg gat acc ttt gca aat gca gga aat tta       354
566  Leu Val Phe Gly Asp Met Thr Asp Thr Phe Ala Asn Ala Gly Asn Leu
567   70                  75                  80                  85
569  gga gat tta gga gct ctg ttg ttt aac aac act aat agc agt aat atc       402
570  Gly Asp Leu Gly Ala Leu Leu Phe Asn Asn Thr Asn Ser Ser Asn Ile
571              90                  95                  100
573  act gat aca gtg ccc gtc atg aat ctg gag gaa gat atg acc agg tat       450
574  Thr Asp Thr Val Pro Val Met Asn Leu Glu Glu Asp Met Thr Arg Tyr
575              105                 110                 115
577  gcc tat tat tac agt gga att ggt gct ggg gtg ctg gtt gct gct tac       498
578  Ala Tyr Tyr Tyr Ser Gly Ile Gly Ala Gly Val Leu Val Ala Ala Tyr
579              120                 125                 130
581  att cag gtt tca ttt tgg tgc ctg gca gct gga aga caa ata cac aaa       546
582  Ile Gln Val Ser Phe Trp Cys Leu Ala Ala Gly Arg Gln Ile His Lys
583              135                 140                 145
585  att aga aaa cag ttt ttt cat gct ata atg cga cag gag ata ggc tgg       594
586  Ile Arg Lys Gln Phe Phe His Ala Ile Met Arg Gln Glu Ile Gly Trp
587  150                 155                 160                 165
589  ttt gat gtg cac gat gtt ggg gag ctt aac acc cgg ctt aca gat gat       642
590  Phe Asp Val His Asp Val Gly Glu Leu Asn Thr Arg Leu Thr Asp Asp
591              170                 175                 180
593  gtc tcc aag att aat gaa gga att ggt gac aaa att gga atg ttc ttt       690
594  Val Ser Lys Ile Asn Glu Gly Ile Gly Asp Lys Ile Gly Met Phe Phe
595              185                 190                 195
597  cag tca atg gca aca ttt ttc act ggg ttt ata gta gga ttt aca cgt       738
598  Gln Ser Met Ala Thr Phe Phe Thr Gly Phe Ile Val Gly Phe Thr Arg
599              200                 205                 210
601  ggt tgg aag cta acc ctt gtg att ttg gcc atc agt cct gtt ctt gga       786
602  Gly Trp Lys Leu Thr Leu Val Ile Leu Ala Ile Ser Pro Val Leu Gly
603              215                 220                 225
605  ctg tca gct gca gtc tgg gca aag ata ctg tct tca ttt act gat aaa       834
606  Leu Ser Ala Ala Val Trp Ala Lys Ile Leu Ser Ser Phe Thr Asp Lys
607  230                 235                 240                 245
609  gaa ctc tta gct tat gca aaa gct gga gca gta gct gaa gag gtc ttg       882
610  Glu Leu Leu Ala Tyr Ala Lys Ala Gly Ala Val Ala Glu Glu Val Leu
611              250                 255                 260
613  gca gca att aga act gtg att gca ttt gga gga caa aag aaa gaa ctc       930
614  Ala Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln Lys Lys Glu Leu
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615              265                270                275
617  gaa agg tac aac aaa aat tta gaa gaa gct aaa aga att ggg ata aag     978
618  Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Arg Ile Gly Ile Lys
619          280                285                290
621  aaa gct att aca gcc aat att tct ata ggt gct gct ttc ctg ctt atc    1026
622  Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala Phe Leu Leu Ile
623          295                300                305
625  tat gca tct tat gct ctg gcc ttc tgg tat ggg acc acc ttg gtc ctc    1074
626  Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr Thr Leu Val Leu
627  310                315                320                325
629  tca aag gaa tat tct att gga caa gta ctc act gta ttc ttt tct gta    1122
630  Ser Lys Glu Tyr Ser Ile Gly Gln Val Leu Thr Val Phe Phe Ser Val
631                  330                335                340
633  tta att ggg gct ttt agt gtt gga cag gca tct cca agc att gaa gca    1170
634  Leu Ile Gly Ala Phe Ser Val Gly Gln Ala Ser Pro Ser Ile Glu Ala
635                  345                350                355
637  ttt gca aat gca aga gga gca gct ttt gaa atc ttc aag ata att gat    1218
638  Phe Ala Asn Ala Arg Gly Ala Ala Phe Glu Ile Phe Lys Ile Ile Asp
639          360                365                370
641  aat aag cca agt att gac agc tat tcg aag agt ggg cac aaa cca gat    1266
642  Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly His Lys Pro Asp
643          375                380                385
645  aat att aag gga aat ttg gaa ttc aga aat gtt cac ttc agt tac cca    1314
646  Asn Ile Lys Gly Asn Leu Glu Phe Arg Asn Val His Phe Ser Tyr Pro
647  390                395                400                405
649  tct cga aaa gaa gtt aag atc ttg aag ggc ctg aac ctg aag gtg cag    1362
650  Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Gln
651                  410                415                420
653  agt ggg cag acg gtg gcc ctg gtt gga aac agc ggc tgt ggg aag agc    1410
654  Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser
655                  425                430                435
657  aca acg gtc cag ctg atg cag agg ctt tat gac ccc aca gag ggc atg    1458
658  Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr Glu Gly Met
659          440                445                450
661  gtc agt gtt gat gga cag gat att agg acc ata aac gta agg ttt cta    1506
662  Val Ser Val Asp Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Phe Leu
663          455                460                465
665  cgg gaa atc atc ggt gtg gtg agt cag gaa cct gta ttg ttt gcc acc    1554
666  Arg Glu Ile Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala Thr
667  470                475                480                485
669  acg ata gct gaa aac att cgc tat ggt cgt gaa gat gtc acc atg gat    1602
670  Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asp Val Thr Met Asp
671  .                490                495                500
673  gag att gag aaa gct gtc aag gaa gcc aat gcc tat gac ttt atc atg    1650
674  Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met
675                  505                510                515
677  aaa ctg cct cag aaa ttt gac acc ctg gtt gga gag aga ggg gcc cag    1698
678  Lys Leu Pro Gln Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln
679          520                525                530
```

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681  ctg agt ggt ggg cag aag cag agg atc gcc att gca cgt gcc ctg gtt     1746
682  Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val
683      535                 540                 545
685  cgc aac ccc aag atc ctc ctg ctg gac gag gcc acg tca gcc ttg gac     1794
686  Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp
687  550                 555                 560                 565
689  aca gaa agt gaa gca gtg gtt cag gtg gct ctg gat aag gcc aga aaa     1842
690  Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu Asp Lys Ala Arg Lys
691                  570                 575                .580
693  ggt cgg acc acc att gtg ata gct cat cgt ttg tct acg gtt cgt aat     1890
694  Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr Val Arg Asn
695          585                 590                 595
697  gcc gac gtc atc gct ggt ttc gat gat gga gtc att gtg gag aaa gga     1938
698  Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile Val Glu Lys Gly
699          600                 605                 610
701  aat cat gat gag ctc atg aaa gag aaa ggc att tac ttc aaa ctt gtc     1986
702  Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe Lys Leu Val
703      615                 620                 625
705  aca atg cag aca gca gga aat gaa att gaa tta gaa aat gca gct gat     2034
706  Thr Met Gln Thr Ala Gly Asn Glu Ile Glu Leu Glu Asn Ala Ala Asp
707  630                 635                 640                 645
709  gaa tcc aaa agt gaa att gat acc ttg gaa atg tct tca cat gat tca     2082
710  Glu Ser Lys Ser Glu Ile Asp Thr Leu Glu Met Ser Ser His Asp Ser
711                  650                 655                 660
713  gga tcc agt cta ata aga aaa aga tcc act cgt agg agt gtc cgt gga     2130
714  Gly Ser Ser Leu Ile Arg Lys Arg Ser Thr Arg Arg Ser Val Arg Gly
715          665                 670                 675
717  tca caa ggc caa gac aga aag ctt agt acc aaa gag gct ctg gat gaa     2178
718  Ser Gln Gly Gln Asp Arg Lys Leu Ser Thr Lys Glu Ala Leu Asp Glu
719          680                 685                 690
721  agt ata cct cca gtt tcc ttt tgg agg att atg aag cta aat tta act     2226
722  Ser Ile Pro Pro Val Ser Phe Trp Arg Ile Met Lys Leu Asn Leu Thr
723      695                 700                 705
725  gag tgg cct tat ttt gtt gtt ggt gta ttt tgt gcc att ata aat gga     2274
726  Glu Trp Pro Tyr Phe Val Val Gly Val Phe Cys Ala Ile Ile Asn Gly
727  710                 715                 720                 725
729  ggt ctg caa cca gca ttt gca gta ata ttt tca aag att ata ggg att     2322
730  Gly Leu Gln Pro Ala Phe Ala Val Ile Phe Ser Lys Ile Ile Gly Ile
731                  730                 735                 740
733  ttt aca aga aat gat gat gcc gaa aca aaa cga cag aat agt aac ttg     2370
734  Phe Thr Arg Asn Asp Asp Ala Glu Thr Lys Arg Gln Asn Ser Asn Leu
735          745                 750                 755
737  ttt tca cta ttg ttt cta gtc ctt gga att gtt tct ttt att aca ttt     2418
738  Phe Ser Leu Leu Phe Leu Val Leu Gly Ile Val Ser Phe Ile Thr Phe
739          760                 765                 770
741  ttc ctt cag ggc ttc aca ttt ggc aaa gct gga gag atc ctc acc aag     2466
742  Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly Glu Ile Leu Thr Lys
743      775                 780                 785
745  cgg ctc cga tac atg gtt ttc cga tcc atg ctc aga cag gat gtg agc     2514
```

RAW SEQUENCE LISTING   DATE: 07/28/2003
PATENT APPLICATION: US/10/619,359   TIME: 08:59:07

Input Set : A:\G00307-70020.txt
Output Set: N:\CRF4\07282003\J619359.raw

```
746  Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu Arg Gln Asp Val Ser
747  790                 795             800                 805
749  tgg ttt gat gac cct aaa aac acc act gga gca ttg act acc agg ctc   2562
750  Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala Leu Thr Thr Arg Leu
751                  810                 815                 820
753  gcc aat gat gct gct caa gtt aaa ggg gct ata ggt tcc agg ctt gct   2610
754  Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile Gly Ser Arg Leu Ala
755                  825                 830                 835
757  ata att acc cag aat ata gca aat ctt ggg aca gga ata att ata tcc   2658
758  Ile Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr Gly Ile Ile Ile Ser
759          840                 845                 850
761  tta atc tat ggt tgg caa ctg aca ctg tta ctc tta gca att gta ccc   2706
762  Leu Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu Leu Ala Ile Val Pro
763      855                 860                 865
765  atc att gca ata gca gga gtt gtt gaa atg aaa atg ttg tct gga caa   2754
766  Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys Met Leu Ser Gly Gln
767  870                 875                 880                 885
769  gca ctg aaa gat aag aaa gaa cta gaa ggt gct ggg aag atc gct act   2802
770  Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala Gly Lys Ile Ala Thr
771                  890                 895                 900
773  gaa gca ata gaa aac ttc cga act gtt gtt tct ttg act cag gag cag   2850
774  Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser Leu Thr Gln Glu Gln
775                  905                 910                 915
777  aag ttt gaa cat atg tat gat cag agt ttg cag gta cca tac aga aac   2898
778  Lys Phe Glu His Met Tyr Asp Gln Ser Leu Gln Val Pro Tyr Arg Asn
779          920                 925                 930
781  tct ttg agg aaa gca cac atc ttt gga atc acg ttt tcc ttc acg cag   2946
782  Ser Leu Arg Lys Ala His Ile Phe Gly Ile Thr Phe Ser Phe Thr Gln
783      935                 940                 945
785  gca atg atg tat ttt tcc tat gct gga tgt ttc cgg ttt gga gcc tac   2994
786  Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe Arg Phe Gly Ala Tyr
787  950                 955                 960                 965
789  ttg gtg gca cat agt ctc atg agc ttt gag gat gtt ctg tta gta ttt   3042
790  Leu Val Ala His Ser Leu Met Ser Phe Glu Asp Val Leu Leu Val Phe
791                  970                 975                 980
793  tca gct gtt gtc ttt ggt gcc atg gcc gtg ggg caa gtc agt tca ttt   3090
794  Ser Ala Val Val Phe Gly Ala Met Ala Val Gly Gln Val Ser Ser Phe
795                  985                 990                 995
797  gct cct gac tat gcc aaa gcc aaa gta tca gca gcc cac atc atc atg   3138
798  Ala Pro Asp Tyr Ala Lys Ala Lys Val Ser Ala Ala His Ile Ile Met
799          1000                1005                1010
801  atc att gaa aaa acc cct ttg att gac agc tac agc aca gaa ggc cta   3186
802  Ile Ile Glu Lys Thr Pro Leu Ile Asp Ser Tyr Ser Thr Glu Gly Leu
803      1015                1020                1025
805  aag ccg aac aca ttg gaa gga aat gtc aca ttt aat gaa gtt gta ttc   3234
806  Lys Pro Asn Thr Leu Glu Gly Asn Val Thr Phe Asn Glu Val Val Phe
W--> 807  ⟨030⟩ /030          1035                1040                1045
809  aac tat ccc acc cga ctg gac atc cca gtg ctt cag ggg ctg agc ctg   3282
810  Asn Tyr Pro Thr Arg Leu Asp Ile Pro Val Leu Gln Gly Leu Ser Leu
```

Input Set : A:\G00307-70020.txt
Output Set: N:\CRF4\07282003\J619359.raw

```
 811                 1050              1055              1060
 813   gaa gtg aag aag ggc cag acg ctg gcc ctg gtg ggc agc agt ggc tgt   3330
 814   Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser Gly Cys
 815                 1065              1070              1075
 817   ggg aag agc acg gtg gtc cag ctc ctg gag cgg ttc tat gac ccc ttg   3378
 818   Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg Phe Tyr Asp Pro Leu
 819              1080              1085              1090
 821   gcg ggg aaa gtg ctg ctt gac ggc aaa gaa ata aag caa ctg aat gtt   3426
 822   Ala Gly Lys Val Leu Leu Asp Gly Lys Glu Ile Lys Gln Leu Asn Val
 823          1095              1100              1105
 825   cag tgg ctc cga gca cac ctg ggc atc gtg tcc cag gag ccc atc ctg   3474
 826   Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln Glu Pro Ile Leu
W-->827  (110)/110          1115              1120              1125
 829   ttt gac tgc agc att agt gag aac att gcc tat gga gac aac agc cgg   3522
 830   Phe Asp Cys Ser Ile Ser Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg
 831                 1130              1135              1140
 833   gtg gtg tca cag gaa gag atc gtg agg gca gcc aag gag gcc aat ata   3570
 834   Val Val Ser Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala Asn Ile
 835              1145              1150              1155
 837   cac gcc ttc atc gag tca ctg cct aat aaa tat agc acc aga gta gga   3618
 838   His Ala Phe Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Arg Val Gly
 839          1160              1165              1170
 841   gac aaa gga act cag ctc tct ggt ggc cag aaa caa cgc att gcc ata   3666
 842   Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile
 843          1175              1180              1185
 845   gct cgt gcc ctt gtt aga cag cct cat att ttg ctt ttg gat gaa gcc   3714
 846   Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp Glu Ala
W-->847  (190)/190          1195              1200              1205
 849   aca tca gct ctg gat aca gaa agt gaa aag gtt gtc caa gaa gcc ctg   3762
 850   Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu Ala Leu
 851                 1210              1215              1220
 853   gac aaa gcc aga gaa ggc cgt acc tgc att gtg att gct cac cgc ctg   3810
 854   Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His Arg Leu
 855             1225              1230              1235
 857   tcc acc atc cag aat gca gac tta ata gtg gtg ttt cag aat ggc aga   3858
 858   Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly Arg
 859          1240              1245              1250
 861   gtc aag gag cac ggc aca cat cag cag ctg ctg gca cag aaa ggc atc   3906
 862   Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile
 863          1255              1260              1265
 865   tat ttt tca atg gtc agt gtc cag gct gga gca aag cgc cag t   3949
 866   Tyr Phe Ser Met Val Ser Val Gln Ala Gly Ala Lys Arg Gln
W-->867  (270)/270          1275              1280
 869   gaactgtgac tgtatgagat gttaaatatt ttttaatatt tgtgtttaaa tatggcattt   4009
 870   attcaaagtt aaaaagcaag tacttataga attatgaaga gttatctgtt taacatttcc   4069
 871   tcaaccaagt tcagagtctt cagacactcg taattaaagg aagagagcga gagacatcat   4129
 872   caagtggaga gaaataatgg tttaaattgc attataaatt ttataacaga gttaaagtag   4189
E-->873  attttt                                                            4195 <-insert
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/619,359**

DATE: 07/28/2003
TIME: 08:59:08

Input Set : **A:\G00307-70020.txt**
Output Set: **N:\CRF4\07282003\J619359.raw**

```
L:14  M:270 C: Current Application Number differs, Replaced Current Application No
L:14  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:365 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:4186 SEQ:1
L:807 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:827 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:873 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:4195 SEQ:3
```